

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/920,705A  
Source: IFW/6  
Date Processed by STIC: 5/18/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 05/18/2006

PATENT APPLICATION: US/09/920,705A

TIME: 11:03:06

Input Set : A:\960296.97214 - Sequence Listing.txt

Output Set: N:\CRF4\05182006\I920705A.raw

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3 <110> APPLICANT: Amasino, Richard M.
4     Schomburg, Fritz M.
5     Michaels, Scott D.
6     Patton, David
8 <120> TITLE OF INVENTION: FLORAL INDUCTION GENE
10 <130> FILE REFERENCE: 960296.97214
12 <140> CURRENT APPLICATION NUMBER: 09/920,705A
13 <141> CURRENT FILING DATE: 2001-08-02
15 <150> PRIOR APPLICATION NUMBER: US 60/222,550
16 <151> PRIOR FILING DATE: 2000-08-03
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4593
24 <212> TYPE: DNA
25 <213> ORGANISM: Arabidopsis thaliana
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32 tacggcgata ttgatagaat cacggtgtat tcttcacgag gctttgcgtt tatatactac      180
34 agacatgttg aggaagcagt cgcagccaaa gaggtctctc aaggagcaaa tttgaatgga      240
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86 tttagggttct tcagagaacg caagacagct ttcattgatt attatgagat ggatgatgct 1800
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90 ctccggtcac aagcgccaaa aaaagtaagc actcttgttg catttgattt ttacttttga 1920
92 aaacgctcca gtaaacattt tgtttagttt cataatttgc gtcaaactga tagggctgag 1980
94 ctctgtcttg tgcccctagg agcagtattt actcgtctct atttcattgt agagtaggct 2040
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210 tca aac aat ctt tgg gtc ggt agc cta acg ccg gag acg aca gag tca 96
211 Ser Asn Asn Leu Trp Val Gly Ser Leu Thr Pro Glu Thr Thr Glu Ser
212 20 25 30
214 gat ctg acc gag ttg ttt gga aga tac ggc gat att gat aga atc acg 144
215 Asp Leu Thr Glu Leu Phe Gly Arg Tyr Gly Asp Ile Asp Arg Ile Thr
216 35 40 45
218 gtg tat tct tca cga ggc ttt gcg ttt ata tac tac aga cat gtg gag 192
219 Val Tyr Ser Ser Arg Gly Phe Ala Phe Ile Tyr Tyr Arg His Val Glu
220 50 55 60
222 gaa gca gtc gca gcc aaa gag gct ctt caa gga gca aat ttg aat gga 240
223 Glu Ala Val Ala Ala Lys Glu Ala Leu Gln Gly Ala Asn Leu Asn Gly
224 65 70 75 80
226 agt caa att aag atc gaa tac gca cga ccg gca aaa cct tgt aag agt 288
227 Ser Gln Ile Lys Ile Glu Tyr Ala Arg Pro Ala Lys Pro Cys Lys Ser
228 85 90 95
230 cta tgg gtg ggt gga atc ggc cct aat gtc tcc aag gat gac ctg gag 336
231 Leu Trp Val Gly Gly Ile Gly Pro Asn Val Ser Lys Asp Asp Leu Glu
232 100 105 110
234 gaa gag ttc agc aag ttt ggg aaa atc gag gat ttt agg ttt ctc aga 384
235 Glu Glu Phe Ser Lys Phe Gly Lys Ile Glu Asp Phe Arg Phe Leu Arg
236 115 120 125
238 gaa cgc aag aca gct ttc att gat tat tat gag atg gat gat gct tta 432
239 Glu Arg Lys Thr Ala Phe Ile Asp Tyr Tyr Glu Met Asp Asp Ala Leu
240 130 135 140
242 cag gct aag agc atg aat gga aag cct atg ggt agc ttt ttg cgt 480
243 Gln Ala Lys Ser Met Asn Gly Lys Pro Met Gly Ser Phe Leu Arg
244 145 150 155 160

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248	165 170 175	
250	tct tac gat aac aga aat ggc aat atg aat cat aaa ccg cag tat cct	576
251	Ser Tyr Asp Asn Arg Asn Gly Asn Met Asn His Lys Pro Gln Tyr Pro	
252	180 185 190	
254	cac tca tat gaa gac ttt aaa gga gat gtc cag cca agt aag gtt ctg	624
255	His Ser Tyr Glu Asp Phe Lys Gly Asp Val Gln Pro Ser Lys Val Leu	
256	195 200 205	
258	tgg att ggg ttc cct cct act gct aca caa tgc aat gat gag caa att	672
259	Trp Ile Gly Phe Pro Pro Thr Ala Thr Gln Cys Asn Asp Glu Gln Ile	
260	210 215 220	
262	ctg cac aat gcg atg ata ctc ttt ggt gag atc gag agg gta aaa agt	720
263	Leu His Asn Ala Met Ile Leu Phe Gly Glu Ile Glu Arg Val Lys Ser	
264	225 230 235 240	
266	tac cca tca agg aat ttt gca ctt gtg gag ttt agg agc gcg gag gaa	768
267	Tyr Pro Ser Arg Asn Phe Ala Leu Val Glu Phe Arg Ser Ala Glu Glu	
268	245 250 255	
270	gct cgc caa tgc aag gaa ggc cta cag ggg agg tta ttc aat aat cct	816
271	Ala Arg Gln Cys Lys Glu Gly Leu Gln Gly Arg Leu Phe Asn Asn Pro	
272	260 265 270	
274	aga atc aaa att atg tac tca aac gat gag ttg cct cct gag caa gac	864
275	Arg Ile Lys Ile Met Tyr Ser Asn Asp Glu Leu Pro Pro Glu Gln Asp	
276	275 280 285	
278	gat act agt ttt tac tct ggt atg aaa cgg tca agg aca gat atg ttc	912
279	Asp Thr Ser Phe Tyr Ser Gly Met Lys Arg Ser Arg Thr Asp Met Phe	
280	290 295 300	
282	aat aat gat cct tca tgt gta tct tct cct cat tct act gga att cct	960
283	Asn Asn Asp Pro Ser Cys Val Ser Ser Pro His Ser Thr Gly Ile Pro	
284	305 310 315 320	
286	ggg tct atg agg ccc ctc aga ggt acg aat gag cgt tca tat aat ggt	1008
287	Gly Ser Met Arg Pro Leu Arg Gly Thr Asn Glu Arg Ser Tyr Asn Gly	
288	325 330 335	
290	gca gaa tac aat gac gtt gtt ggt aag gag cca aac tgg agg agg cca	1056
291	Ala Glu Tyr Asn Asp Val Val Gly Lys Glu Pro Asn Trp Arg Arg Pro	
292	340 345 350	
294	tct gca aat gga act gga ata ctc cca tct cca aca gga cct gga atc	1104
295	Ser Ala Asn Gly Thr Gly Ile Leu Pro Ser Pro Thr Gly Pro Gly Ile	
296	355 360 365	
298	ctc cca tct cct gca caa ggt acg agg cgc cct atg agg tca aac ccc	1152
299	Leu Pro Ser Pro Ala Gln Gly Thr Arg Arg Pro Met Arg Ser Asn Pro	
300	370 375 380	
302	gat tct tgg gaa gga tat gat cct gct cag ttg gtc aga gaa agt aaa	1200
303	Asp Ser Trp Glu Gly Tyr Asp Pro Ala Gln Leu Val Arg Glu Ser Lys	
304	385 390 395 400	
306	cga acc aga aga gat gga tca gtg gac ggt ttt act cca atg ggt gtc	1248
307	Arg Thr Arg Arg Asp Gly Ser Val Asp Gly Phe Thr Pro Met Gly Val	
308	405 410 415	
310	gat gag agg tca ttt ggt cga ggt tca gtt gct gct aga cct atc cgt	1296

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314	ggc	ccc	cct	gat	tct	gat	cac	ata	tgg	aga	gga	atg	att	gcc	aag	ggc	1344
315	Gly	Pro	Pro	Asp	Ser	Asp	His	Ile	Trp	Arg	Gly	Met	Ile	Ala	Lys	Gly	
316				435					440					445			
318	gga	act	ccc	gtc	tgt	tgt	gct	cgt	tgt	gta	cct	atg	gga	aag	ggg	att	1392
319	Gly	Thr	Pro	Val	Cys	Cys	Ala	Arg	Cys	Val	Pro	Met	Gly	Lys	Gly	Ile	
320		450					455						460				
322	gaa	act	aaa	ctg	cct	gag	gtc	gtc	aat	tgt	tca	gca	aga	act	gat	ttg	1440
323	Glu	Thr	Lys	Leu	Pro	Glu	Val	Val	Asn	Cys	Ser	Ala	Arg	Thr	Asp	Leu	
324	465						470					475				480	
326	aat	atg	ctc	gct	aaa	cat	tac	gcc	gtt	gcc	att	gga	tgt	gag	atc	gtt	1488
327	Asn	Met	Leu	Ala	Lys	His	Tyr	Ala	Val	Ala	Ile	Gly	Cys	Glu	Ile	Val	
328					485					490					495		
330	ttt	ttc	gta	cca	gac	agg	gaa	gaa	gat	ttt	gcg	tct	tac	act	gaa	ttt	1536
331	Phe	Phe	Val	Pro	Asp	Arg	Glu	Glu	Asp	Phe	Ala	Ser	Tyr	Thr	Glu	Phe	
332				500					505					510			
334	ctc	cgg	tac	ctt	agc	tca	aaa	gat	cgg	gcg	ggc	gtt	gcc	aaa	tta	gat	1584
335	Leu	Arg	Tyr	Leu	Ser	Ser	Lys	Asp	Arg	Ala	Gly	Val	Ala	Lys	Leu	Asp	
336			515					520					525				
338	gat	ggc	aca	act	tta	ttc	ttg	gtg	cct	cca	tca	gat	ttc	tta	act	gat	1632
339	Asp	Gly	Thr	Thr	Leu	Phe	Leu	Val	Pro	Pro	Ser	Asp	Phe	Leu	Thr	Asp	
340		530					535						540				
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343	Val	Leu	Gln	Val	Thr	Arg	Gln	Glu	Arg	Leu	Tyr	Gly	Val	Val	Leu	Lys	
344	545					550					555					560	
346	tta	ccc	ccg	cca	gcc	gtt	cct	gtt	aca	gca	tca	tac	aga	caa	gaa	tct	1728
347	Leu	Pro	Pro	Pro	Ala	Val	Pro	Val	Thr	Ala	Ser	Tyr	Arg	Gln	Glu	Ser	
348				565						570					575		
350	cag	tcc	aat	cct	ctg	cat	tat	atg	gat	caa	gcc	cgg	gat	tca	cct	gcc	1776
351	Gln	Ser	Asn	Pro	Leu	His	Tyr	Met	Asp	Gln	Ala	Arg	Asp	Ser	Pro	Ala	
352				580					585					590			
354	aat	gct	agt	cac	agt	tta	tat	cct	cct	agg	gaa	aat	tac	att	agg	ggc	1824
355	Asn	Ala	Ser	His	Ser	Leu	Tyr	Pro	Pro	Arg	Glu	Asn	Tyr	Ile	Arg	Gly	
356			595					600					605				
358	gca	cca	gaa	cat	ttg	aca	gct	gct	tca	aaa	cca	tct	gtt	agc	gag	cct	1872
359	Ala	Pro	Glu	His	Leu	Thr	Ala	Ala	Ser	Lys	Pro	Ser	Val	Ser	Glu	Pro	
360		610					615						620				
362	ctc	aga	ata	cct	aat	aat	gca	gcg	cct	caa	gct	ggg	gtt	agt	tta	act	1920
363	Leu	Arg	Ile	Pro	Asn	Asn	Ala	Ala	Pro	Gln	Ala	Gly	Val	Ser	Leu	Thr	
364	625					630					635					640	
366	ccg	gag	ctt	tta	gcc	act	ctg	gca	tct	att	ctc	cct	gca	act	tct	caa	1968
367	Pro	Glu	Leu	Leu	Ala	Thr	Leu	Ala	Ser	Ile	Leu	Pro	Ala	Thr	Ser	Gln	
368				645					650					655			
370	cct	gct	gcc	cct	gag	agt	cac	caa	cct	atg	tca	gga	cct	tca	aca	gtt	2016
371	Pro	Ala	Ala	Pro	Glu	Ser	His	Gln	Pro	Met	Ser	Gly	Pro	Ser	Thr	Val	
372			660						665					670			
374	gtt	tcc	aca	gca	cat	cag	tcc	aat	gga	ctg	tac	aat	gga	gaa	gca	ccg	2064
375	Val	Ser	Thr	Ala	His	Gln	Ser	Asn	Gly	Leu	Tyr	Asn	Gly	Glu	Ala	Pro	

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10

**VERIFICATION SUMMARY**

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